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Editorial

Hypervirulent *Klebsiella pneumoniae*: Liver Abscess Isolates versus Intestinal Flora

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▸ See the article "Characteristics of *Klebsiella pneumoniae* Isolates from Stool Samples of Patients with Liver Abscess Caused by Hypervirulent *K. pneumoniae*" in volume 35, number 2, e18.

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Serotype K1 *Klebsiella pneumoniae* strains, which are hypervirulent and mostly belong to sequence type 23 by multilocus sequence typing, have been a major cause of community-acquired liver abscess in Asian countries including Taiwan and Korea during the past 3 decades.[1] Interestingly, the strain of this serotype was rarely found in infections among patients in western countries despite that it was known to be highly virulent. The cause of this difference between Asian and western countries has not yet been clearly identified, however, subsequent studies have shown that this clone was found to be among intestinal microbiota in a substantial proportion of healthy adults in Asian countries including Korea, Taiwan and China.[2,3] The findings of a previous study that a much lower proportion of the foreigners of Korean ethnicity who had lived in the countries other than Korea carried serotype K1 *K. pneumoniae* strain suggested environmental factors as a possible cause for explaining geographical differences in the global epidemiology of *K. pneumoniae* liver abscess.

K. pneumoniae can normally colonize the intestinal tract and oropharynx of healthy adults, and intestinal colonization has been suggested to precede invasion of the intestinal mucosa and portal venous flow or ascending biliary infection followed by the development of liver abscess. Kim et al.'s[4] report in the present issue provided information on the concordance between the *K. pneumoniae* liver aspirate isolates and *K. pneumoniae* fecal isolates from the liver abscess patients and suggested that there is significant heterogeneity of *K. pneumoniae* colonizing intestinal tract of the hypervirulent *K. pneumoniae* liver abscess patients in Korea. In this study, concordance rate was only 27.3% and the majority of the *K. pneumoniae* fecal isolates belonged to serotype non-K1/K2. This low concordance rate contrasts with a previous study in Taiwan, reporting that 10 patients among 43 patients with *K. pneumoniae* liver abscess showed identical serotypes and genotypes with the same virulence.[5]

This discrepancy between studies appears to be due to differences in timing of sampling of stool samples in hospitalized patients with liver abscess. Although a previous study from Taiwan described that stool samples were collected before starting antibiotic therapy, this study mentioned that the median time between initiation of antibiotic therapy in patients with liver abscess and collection of stool samples was 14 days. Intestinal microbiota could change by antibiotic therapy and could affect the results of this study. The findings in this

study that all of 8 *K. pneumoniae* fecal isolates belonging to serotype non-K1/K2 were extended spectrum beta-lactamase (ESBL)-producers and 75% were ciprofloxacin-resistant suggest the possibility that many of *K. pneumoniae* fecal isolates in this study might not be actually the etiologic intestinal flora preceding invasion to the liver and could be acquired later and selected by antibiotic pressure.

Another possibility explaining such a discrepancy in studies is differences in methods for isolation and identification of *K. pneumoniae* strains from stool samples. *K. pneumoniae* is known to be isolated from stool in around one third of healthy adults using the conventional microbiological culture techniques, however the yield can be affected by the sort of culture media and the experience and expertise of the laboratory technician. In fact, culture-based studies investigating intestinal microbiota are known to give only a limited view of diverse and complex microbiota.

Recent progress in culture-independent microbiome research will be helpful in further understanding of *K. pneumoniae* epidemiology in both patients with liver abscess and healthy persons. Further research is required to understand better geographical differences in *K. pneumoniae* epidemiology.

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